



SEQUENCE LISTING

<110> KATO, Seishi  
KIMURA, Tomoko

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 2003-0984/WMC/01791

<140> 10/019,151

<141> 2003-01-31

<150> JP 11-178065

<151> 1999-06-24

<160> 24

<210> 1

<211> 238

<212> PRT

<213> Homo sapiens

<400> 1

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val Asp Met  
1 5 10 15

Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly  
20 25 30

Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr  
35 40 45

Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val  
50 55 60

Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu  
65 70 75 80

Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly  
85 90 95

Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile  
100 105 110

Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe  
115 120 125

Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His  
130 135 140

Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu  
145 150 155 160

Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val  
165 170 175

Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile  
180 185 190

Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala  
195 200 205

Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly  
210 215 220

Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser  
 225 230 235

<210> 2  
 <211> 339  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu  
 1 5 10 15  
 Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn  
 20 25 30  
 Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His  
 35 40 45  
 Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu  
 50 55 60  
 Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val  
 65 70 75 80  
 Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu  
 85 90 95  
 Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val  
 100 105 110  
 Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly  
 115 120 125  
 Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln  
 130 135 140  
 Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp  
 145 150 155 160  
 Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu  
 165 170 175  
 Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu  
 180 185 190  
 Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro  
 195 200 205  
 Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro  
 210 215 220  
 Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His  
 225 230 235 240  
 Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr  
 245 250 255  
 Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile  
 260 265 270  
 Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp  
 275 280 285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn  
 290 295 300  
 Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys  
 305 310 315 320  
 Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr  
 325 330 335  
 Arg Arg Arg

<210> 3  
 <211> 326  
 <212> PRT  
 <213> Homo sapiens

<400> 3  
 Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr Leu  
 1 5 10 15  
 Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr Thr Ser  
 20 25 30  
 Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val Pro Lys Pro  
 35 40 45  
 Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser  
 50 55 60  
 Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn  
 65 70 75 80  
 Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly  
 85 90 95  
 Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys  
 100 105 110  
 Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp  
 115 120 125  
 Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln Phe Ile Ser  
 130 135 140  
 Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys  
 145 150 155 160  
 Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly  
 165 170 175  
 Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala  
 180 185 190  
 Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr  
 195 200 205  
 Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala  
 210 215 220  
 Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe  
 225 230 235 240



210		215		220
Pro Gln Lys Lys Trp	Leu His Phe Ile Ser	Pro Ile Phe Val Gln Ala		
225	230	235	240	
Leu Thr Leu Thr Phe	Leu Ala Glu Trp Gly	Asp Arg Ser Gln Leu Thr		
	245	250	255	
Thr Ile Val Leu Ala Ala Arg Glu	Asp Pro Tyr Gly Val Ala Val Gly			
	260	265	270	
Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly				
	275	280	285	
Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly				
	290	295	300	
Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro				
305	310	315	320	

Asp Ser Gly Phe

<210> 5  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 5	
Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val	
1	5 10 15
Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu	
	20 25 30
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val	
	35 40 45
Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu	
	50 55 60
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala	
	65 70 75 80
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr	
	85 90 95
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu	
	100 105 110
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr	
	115 120 125
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly	
	130 135 140
Val Arg Ile Phe Gly Ile Asn Lys Tyr	
145	150

<210> 6  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val  
1 5 10 15  
Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu  
20 25 30  
Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val  
35 40 45  
Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu  
50 55 60  
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala  
65 70 75 80  
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr  
85 90 95  
Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu  
100 105 110  
Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr  
115 120 125  
Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly  
130 135 140  
Val Arg Val Phe Gly Ile Asn Lys Tyr  
145 150

<210> 7

<211> 200

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala  
1 5 10 15  
Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp  
20 25 30  
Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe  
35 40 45  
Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg  
50 55 60  
Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu  
65 70 75 80  
Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val  
85 90 95  
Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe  
100 105 110  
Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser  
115 120 125  
Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val  
130 135 140

Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys  
 145 150 155 160  
 Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met  
 165 170 175  
 Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr  
 180 185 190  
 Leu Glu Lys Thr Ile His Glu Glu  
 195 200

<210> 8  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala  
 1 5 10 15  
 Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro  
 20 25 30  
 Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu  
 35 40 45  
 Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu  
 50 55 60  
 Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg  
 65 70 75 80  
 Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser  
 85 90 95  
 Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg  
 100 105 110  
 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val  
 115 120 125  
 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu  
 130 135 140  
 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln  
 145 150 155 160  
 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly  
 165 170 175  
 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu  
 180 185

<210> 9  
 <211> 714  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 atgattctgc ttgtgattct tgcattttat ctgtggcagg tggacatggt gagtgaaatt 60  
 7

aacattgctc	cccgattctt	caccaatttc	actggagtaa	tgccacctca	gttcaaaaag	120
gatttggtt	cctatcttaa	aactcgatca	ccagtcactt	tcctgtctga	tctgctgcagc	180
aacctacagg	tatccaatga	acctgggaat	cgctacaacc	tccagctcat	caatgcactg	240
gtgctctatg	tcgggactca	ggccattgcg	cacatccaca	acaagggcag	cacaccttca	300
atgagcacca	tcactcactc	agcacacatg	gatatcttcc	agaatttggc	tgtggacttg	360
gacactgagg	gtcgctatct	ctttttgaat	gcaattgcaa	atcagctccg	gtacccaaat	420
agccacactc	actacttcag	ttgcaccatg	ctgtaccttt	ttgcagaggc	caatacggaa	480
gccatccaag	aacagatcac	aagagttctc	ttggaacggg	tgattgtaaa	taggccacat	540
ccttgggggtc	ttcttattac	cttcattgag	ctgattaaaa	acccagcggt	taagttctgg	600
aaccatgaat	ttgtacactg	tgccccagaa	atcgaaaagt	tattccagtc	ggtcgcacag	660
tgctgcatgg	gacagaagca	ggcccagcaa	gtaatggaag	ggacaggtgc	cagt	714

<210> 10  
 <211> 1017  
 <212> DNA  
 <213> Homo sapiens

<400> 10						
atggccgcag	cctgcggggc	gggagcggcc	gggtactgct	tgctcctcgg	cttgcathtt	60
tttctgctga	ccgcggggcc	tgccctgggc	tggaacgacc	ctgacagaat	gttgctgcgg	120
gatgtaaaag	ctcttaccct	ccactatgac	cgctatacca	cctcccgag	gctggatccc	180
atccccagtg	tgaaatgtgt	tgagggcaca	gctggttgtg	attcttatac	cccaaaagtc	240
atacagtgtc	agaacaaagg	ctgggatggg	tatgatgtac	agtgggaatg	taagacggac	300
ttagatattg	catacaaat	tggaaaaact	gtggtgagct	gtgaaggcta	tgagtctctt	360
gaagaccagt	atgtactaag	aggttcttgt	ggcttgaggt	ataatttaga	ttatacagaa	420
cctggcctgc	agaaactgaa	ggagtctgga	aagcagcacg	gctttgcctc	tttctctgat	480
tattattata	agtggctctc	ggcggattcc	tgtaacatga	gtggattgat	taccatcgtg	540
gtactccttg	ggatcgcttc	tgtagtctat	aagctgttcc	tgagtgcgg	gcagtattct	600
cctccaccgt	actctgagta	tcctccattt	tcccaccgtt	accagagatt	caccaactca	660
gcaggacctc	ctcccccagg	ctttaagtct	gagttcacag	gaccacagaa	tactggccat	720
ggtgcaactt	ctggttttgg	cagtgccttt	acaggacaac	aaggatatga	aaattcagga	780
ccagggttct	ggacaggctt	gggaactggt	ggaatactag	gatatttggt	tggcagcaat	840
agagcggcaa	cacccttctc	agactcgtgg	tactaccctg	cctatcctcc	ctcctaccct	900
ggcacgtgga	atagggtcta	ctcaccctt	catggaggct	cgggcagcta	ttcggtatgt	960
tcaaactcag	acacgaaaaac	cagaactgca	tcaggatatg	gtggtaccag	gagacga	1017

<210> 11  
 <211> 978  
 <212> DNA  
 <213> Homo sapiens

<400> 11						
atggccaaga	tggagctctc	gaaggccttc	tctggccagc	ggacactcct	atctgccatc	60
ctcagcatgc	tatcactcag	cttctccaca	acatccctgc	tcagcaacta	ctggtttgtg	120
ggcacacaga	aggtgcccaa	gcccctgtgc	gagaaaagtc	tggcagccaa	gtgctttgac	180
atgccagtgt	ccctggatgg	agataccaac	acatccaccc	aggagggtgt	acaatacaac	240
tgggagactg	gggatgaccg	gttctccttc	cggagcttcc	ggagtggcat	gtggctatcc	300
tgtgaggaag	ctgtggaaga	accaggggag	aggtgccgaa	gtttcattga	acttacacca	360
ccagccaaga	gagaaatcct	atggttatcc	ctgggaacgc	agatcaccta	catcgactt	420
caattcatca	gcttctctct	gctactaaca	gacttgctac	tcactgggaa	ccctgcctgt	480
gggctcaaac	tgagcgcttt	tgctgctgtt	tcctctgtcc	tgtcaggctc	cctggggatg	540
gtggcccaca	tgatgtattc	acaagtcttc	caagcgactg	tcaacttggg	tccagaagac	600
tggagaccac	atgtttggaa	ttatggctgg	gccttctaca	tggcctggct	ctccttcacc	660
tgctgcatgg	cgctggctgt	caccaccttc	aacacgtaca	ccaggatggt	gctggagttc	720
aagtgaagc	atagtaagag	cttcaaggaa	aacccgaact	gcctaccaca	tcaccatcag	780
tgtttccctc	ggcggctgtc	aagtgcagcc	cccaccgtgg	gtcctttgac	cagctaccac	840
cagatcatata	atcagcccat	ccactctgtc	tctgagggag	tcgacttcta	ctccgagctg	900
cgaacaagg	gatttcaaag	aggggcccagc	caggagctga	aagaagcagt	taggtcatct	960
gtagaggaag	agcagtgt					978

<210> 12

<211> 972  
 <212> DNA  
 <213> Homo sapiens

<400> 12  
 atggcgccg cggctccggg gaacggccgc gcatcgccgc cccggctgct tctgctcttt 60  
 ctggttccgc tgctgtgggc cccggctgcg gtccgggccc gccagatga agaccttagc 120  
 caccggaaca aagaaccgcc ggcgccggcc cagcagctgc agccgcagcc tgtggctgtg 180  
 cagggccccc agccggcccc ggctcgagaaa atatttacac cagcagctcc agttcatacc 240  
 aataaagaag atcctgctac ccaaactaat ttgggattta tccatgcatt tctcgtgcc 300  
 atatcagtta ttattgtatc tgaattgggt gataagacat tttttatagc agccatcatg 360  
 gcaatgcgct ataaccgcct gaccgtgctg gctgggtgcaa tgcttgccctt gggactaatg 420  
 acatgcttgt cagttttgtt tggctatgcc accacagtca tccccagggt ctatacatc 480  
 tatgtttcaa ctgtattatt tgccattttt ggcattagaa tgcttcggga aggcttaaag 540  
 atgagccctg atgagggtca agaggaactg gaagaagttc aagctgaatt aaagaagaaa 600  
 gatgaagaat ttcaacgaac caaactttta aatggaccgg gagatgttga aacgggtaca 660  
 agcataacag tacctcagaa aaagtgggtg cattttattt caccattttt tgttcaagct 720  
 cttacattaa cattcttagc agaattgggt gatcgctctc aactaactac aattgtattg 780  
 gcagctagag aggaccctta tgggttagcc gtgggtggaa ctgtggggca ctgcctgtgc 840  
 acgggatttg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg 900  
 acaatcatag gaggcacgtt ttttttggcg tttgcatttt ctgcactatt tataagccct 960  
 gattctggtt tt 972

<210> 13  
 <211> 459  
 <212> DNA  
 <213> Homo sapiens

<400> 13  
 atgaatgtgg gcacagcgca cagcgaggtg aaccccaaca cgcgggtgat gaacagccgt 60  
 ggcattctggc tctcctacgt gctggccatc ggtctcctcc acatcgtgct gctgagcatc 120  
 ccgtttgtga gtgtccctgt cgtctggacc ctccaccaacc tcatccacaa catgggcatg 180  
 tatatcttcc tgcacacggg gaaggggaca ccctttgaga ccccgacca gggcaaggcg 240  
 aggtgtctaa cccactggga gcagatggat tatgggtccc agttcacggc ctctcggaag 300  
 ttcttgacca ccacacccat cgtgctgtac ttcctcacca gcttctacac taagtacgac 360  
 cagatccatt ttgtgtctca caccgtgtcc ctgatgagcg tgcttatccc caagctgccc 420  
 cagctccacg gagtccggat ttttgggaatc aataagtac 459

<210> 14  
 <211> 459  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
 atgaatgtgg ggggtggcaca cagcgaagta aaccccaaca cccgagtgat gaatagccga 60  
 ggcattctggc tggcctacat catcttggta ggattgctgc atatggttct actcagcatc 120  
 cccttcttca gcattcctgt tgtctggacc ctgaccaacg tcatccataa cctggctacg 180  
 tatgtcttcc ttcatacggg gaaagggaca ccctttgaga ctctgacca aggaaaggct 240  
 cggctactga cacactggga gcaaattggac tatgggtccc agtttacctc ttcccgcaag 300  
 ttctctagca tctctcctat tgtgctctat ctcttgcca gcttctatac caagtatgat 360  
 gctgcgcaact tctcatcaa cacagcctca ttgctaagtg tactgctgcc gaagttgccc 420  
 cagttccatg gggttcgtgt ctttggcatc aacaaatac 459

<210> 15  
 <211> 600  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
 atggcagcat ctatgcatgg tcagcccagt ctttctctag aagatgcaaa actcagaaga 60  
 ccaatggtca tagaaatcat agaaaaaat tttgactatc ttagaaaaga aatgacacaa 120



ctc	ttt	ttg	aat	gca	att	gca	aat	cag	ctc	cgg	tac	cca	aat	agc	cac	612
Leu	Phe	Leu	Asn	Ala	Ile	Ala	Asn	Gln	Leu	Arg	Tyr	Pro	Asn	Ser	His	
			130					135					140			
act	cac	tac	ttc	agt	tgc	acc	atg	ctg	tac	ctt	ttt	gca	gag	gcc	aat	660
Thr	His	Tyr	Phe	Ser	Cys	Thr	Met	Leu	Tyr	Leu	Phe	Ala	Glu	Ala	Asn	
		145					150					155				
acg	gaa	gcc	atc	caa	gaa	cag	atc	aca	aga	gtt	ctc	ttg	gaa	cgg	ttg	708
Thr	Glu	Ala	Ile	Gln	Glu	Gln	Ile	Thr	Arg	Val	Leu	Leu	Glu	Arg	Leu	
	160					165					170					
att	gta	aat	agg	cca	cat	cct	tgg	ggg	ctt	ctt	att	acc	ttc	att	gag	756
Ile	Val	Asn	Arg	Pro	His	Pro	Trp	Gly	Leu	Leu	Ile	Thr	Phe	Ile	Glu	
	175				180				185						190	
ctg	att	aaa	aac	cca	gcg	ttt	aag	ttc	tgg	aac	cat	gaa	ttt	gta	cac	804
Leu	Ile	Lys	Asn	Pro	Ala	Phe	Lys	Phe	Trp	Asn	His	Glu	Phe	Val	His	
			195					200				205				
tgt	gcc	cca	gaa	atc	gaa	aag	tta	ttc	cag	tcg	gtc	gca	cag	tgc	tgc	852
Cys	Ala	Pro	Glu	Ile	Glu	Lys	Leu	Phe	Gln	Ser	Val	Ala	Gln	Cys	Cys	
		210					215					220				
atg	gga	cag	aag	cag	gcc	cag	caa	gta	atg	gaa	ggg	aca	ggg	gcc	agt	900
Met	Gly	Gln	Lys	Gln	Ala	Gln	Gln	Val	Met	Glu	Gly	Thr	Gly	Ala	Ser	
	225					230					235					
tagacgaaac	tgcatctctg	ttgtacgtgt	cagtctagag	gtctcactgc	accgagttca	960										
taaactgact	gaagaatcct	ttcagctctt	cctgactttc	ccagcccttt	ggtttggtggg	1020										
tatctgcccc	aactactgtt	gggatcagcc	tcctgtctta	tgtgggcacg	ttccaaagtt	1080										
taaatgcatt	tttttgactc	ttggccaaaa	tttagaagat	gctgtgaata	tcattttgaa	1140										
cttgtgtaaa	tacatgaaag	agaaaac				1167										

<210> 18  
 <211> 1925  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (115)... (1134)

<400> 18	
gttccttcgc	cgccgccagg
cccagggttcg	gcccgtaggc
	gtctggcagc
	ccggcgccat
	cttcacgcag
	cgcc atg
	Met
	1
gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc	165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly	
	5
ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac	213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp	
	20
cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat	261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr	
	35
gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa	309
Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys	
	50
tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata	357
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile	
	70
cag tgt cag aac aaa ggc tgg gat ggg gat gta cag tgg gaa tgt	405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys	
	85
aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc	453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser	
	100
	105
	110

tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct	501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser	
115 120 125	
tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa	549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys	
130 135 140 145	
ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat	597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr	
150 155 160	
tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att	645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile	
165 170 175	
acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc	693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe	
180 185 190	
ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca	741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro	
195 200 205	
ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc	789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro	
210 215 220 225	
cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt	837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly	
230 235 240	
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa	885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu	
245 250 255	
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta	933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Ile Leu	
260 265 270	
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg	981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser	
275 280 285	
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg	1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg	
290 295 300 305	
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca	1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser	
310 315 320	
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg	1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg	
325 330 335	
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatttt	1180
Arg Arg	

tcatcacttt ctcttttagaa aaaaagtact acctgttaac aattgggaaa aggggatatt	1240
caaaagttct gtggtgttat gtccagtgtta gctttttgta ttctattatt tgaggctaaa	1300
agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt	1360
gcagtttttg aaagtgatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct	1420
gtgatgccct aagaagcatt aagaatgaag gtgtgtgact aatagaaact aagtacagaa	1480
aatttcagtt ttaggtggtt gtagctgatg agttattacc tcatagagac tataatattc	1540
tatttggtat tatattattt gatgtttgct gttcttcaaa catttaaatc aagctttgga	1600
ctaattatgc taatttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca	1660
gtggtggaga tggccttctg gtaactgaat attaccttct gtaggaaaag gtggaaaata	1720
agcatctaga aggttgttgt gaatgactct gtgctggcaa aaatgcttga aacctctata	1780
tttctttcgt tcataagagg taaagggtcaa atttttcaac aaaagtcttt taataacaaa	1840
agcatgcagt tctctgtgaa atctcaaata ttgttgtaat agtctgtttc aatcttaaaa	1900
agaatcaata aaaacaaaca agggg	1925

<210> 19  
 <211> 1125  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (71) ... (1051)

<400> 19  
 ttaaaccaaa gggacttggga gtgcagatgg catccttcgg ttcttccaga caagctgcaa 60  
 gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109  
                   Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln  
                   1                  5                  10  
 cgga aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157  
 Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser  
           15                  20                  25  
 aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205  
 Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val  
           30                  35                  40                  45  
 ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg 253  
 Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met  
                   50                  55                  60  
 cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag gtg gta 301  
 Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val  
                   65                  70                  75  
 caa tac aac tgg gag act ggg gat gac cgg ttc tcc ttc cgg agc ttc 349  
 Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe  
                   80                  85                  90  
 cgg agt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg 397  
 Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly  
           95                  100  
 gag agg tgc cga agt ttc att gaa ctt aca cca gcc aag aga gaa 445  
 Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu  
           110                  115                  120                  125  
 atc cta tgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa 493  
 Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln  
                   130                  135  
 ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac 541  
 Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn  
                   145                  150                  155  
 cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc 589  
 Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val  
                   160                  165                  170  
 ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc 637  
 Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val  
           175                  180                  185  
 ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685  
 Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val  
           190                  195                  200                  205  
 tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733  
 Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys  
                   210                  215                  220  
 tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg 781  
 Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val  
                   225                  230                  235  
 ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829  
 Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn  
                   240                  245                  250  
 tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca 877  
 Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala  
                   255                  260                  265  
 gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag 925  
 Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln  
           270                  275                  280                  285  
 ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg 973  
 Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg  
                   290                  295                  300

aac aag gga ttt caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt	1021
Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val	
305 310 315	
agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg	1070
Arg Ser Ser Val Glu Glu Glu Gln Cys	
320 325	
agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc	1125

<210> 20  
 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (40) ... (1014)

<400> 20	
ctcttgccggc gcccgtgctg gcgccggcccg gcaggcgagg atg gcg gcc gcg gct	54
Met Ala Ala Ala Ala	
1 5	
ccg ggg aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg	102
Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu	
10 15 20	
gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa	150
Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu	
25 30 35	
gac ctt agc cac cgg aac aaa gaa ccg gcg ccg gcc cag cag ctg	198
Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu	
40 45 50	
cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag	246
Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu	
55 60 65	
aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cct	294
Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro	
70 75 80 85	
gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata	342
Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile	
90 95 100	
tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca	390
Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala	
105 110 115	
gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca	438
Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala	
120 125 130	
atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat	486
Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr	
135 140 145	
gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta	534
Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val	
150 155 160 165	
tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg	582
Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met	
170 175 180	
agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta	630
Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu	
185 190 195	
aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg	678
Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro	
200 205 210	
gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg	726
Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp	
215 220 225	

ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc	774
Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe	
230 235 240 245	
tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca	822
Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala	
250 255 260	
gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac	870
Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His	
265 270 275	
tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag	918
Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln	
280 285 290	
aaa atc tct gtc aga act gtg aca atc ata gga ggc atc gtt ttt ttg	966
Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu	
295 300 305	
gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt	1011
Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe	
310 315 320	
taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat	1070
agtgtacatt acaactaaaa gtgatggaaa aatactgtat tttgtagcac tgattttgtg	1130
agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt	1190
taaaagaacac ctgacttcta agtgtgggtt tttcttctct ccaacataat tatgttaata	1250
tggtcctcat ttttcttttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt	1310
ctttcagcac tgaccccttt ttaaggaata caaattttct cttcatcac ttaggtgttt	1370
taagatgttt accttaaagt ttttcttggg gaaagaatga attaatcttct atttcttaaa	1430
acatttcctt gagccagtaa acagtagttt aatcattggt cttttcaaaa ctaggtgttt	1490
aaaaaaagag acatatatga tattgctgtt atatcaataa catggcacia caagaactgt	1550
ctgccaggctc attcttcctc tttttttttt aattgggtag gacacccaat ataaaaacag	1610
tcaatatattg acaatgtgga attaccaaat taaaagagaa tactatgaat gtattcatat	1670
tttttctata ttgaataaac aatgtaacat agataacaat ataaataaaa gtgggtatgac	1730
cagt	1734

<210> 21  
 <211> 2064  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (98) ... (559)

<400> 21	
aaaacagctg ctggagcagc agcggccccc gctcccggga accgttcccg ggccgttgat	60
cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca	112
Met Asn Val Gly Thr	
1 5	
gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc	160
Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly	
10 15 20	
atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg	208
Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu	
25 30 35	
ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac	256
Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn	
40 45 50	
ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg	304
Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly	
55 60 65	
aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac	352
Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His	
70 75 80 85	
tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc	400
Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe	
15	

	90	95	100	
ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act				448
Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr				
	105	110	115	
aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc				496
Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser				
	120	125	130	
gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga				544
Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly				
	135	140	145	
atc aat aag tac tgagagtgc gccccttccc ctgcccaggg tggcagggga gggg				600
Ile Asn Lys Tyr				
150				
tagggtaaaa ggcattgtgct gcaacactga agacagaaaag aagaagcctc tggacactgc				660
cagagatggg gggttgagcct ctggcctaata tccccccctc gcttccccca gtagccaact				720
tggagtagct tgtagtgggg ttggggtagg cccccctggc tctgaccttt tctgaatttt				780
ttgatctttt ccttttgctt tttgaataga gactccatgg agttgggtcat ggaatgggct				840
gggctcctgg gctgaacatg gaccacgcag ttgcgacagg aggccagggg aaaaaccctt				900
gctcacttgt ttgccctcag gcagccaaag cactttaacc cctgcatagg gagcagaggg				960
cggtacggct tctggattgt ttcactgtga ttcctagggt ttttcgatgc cacgcagtgt				1020
gtgcttttgt gtatggaagc aagtgtggga tgggtctttg cttttctggg tagggagctg				1080
tctaatacaa gtcccaggct tttggcagct tctctgcaac ccaccgtggg tcctggttgg				1140
gagtggggag ggtcagggtt gggaagaatg gggtagatg tagatggctt ggttccagag				1200
gtgagggggc cagggtgct gccatcctgg cctgggtggag gttggggagc tgtaggagag				1260
ctagtgaagc gagacttaga agaatggggc cacatagcag cagaggactg gtgtaaggga				1320
gggaggggta gggacagaag ctagacccaa tctcctttgg gatgtgggca gggaggggag				1380
caggcttgga gggttaattt acccacagaa tgtgatagta ataggggagg gaggctgctg				1440
tgggtttaac tcctgggttg gctgttgggt agacagggtg ggaaaaggcc cgtgagtcac				1500
tgtaaacaca ggtccaactt ggccctgact cctgcggggg tatgggggag ctgtgacaga				1560
aacgatgggt gctgtgggtc tctgcaggcc ctcacccctt aacttcctca tacagactgg				1620
cactgggcag ggcctctcat gtggcagcca catgtggcgt tgtgaggcca ccccatgtgg				1680
ggtctgtggt gagagtcctg taggatccct gctcaagcag cacagaggaa ggggcaagac				1740
gtggcctgta ggcactgttt cagcctgcag agaagaaagt gaggccggga gcctgagcct				1800
gggctggagc cttctccctt ccccagtttg actaggggca gtgttaattt tgaaaagggtg				1860
tgggtccctg tgcctcttc cagggttcca agggaacagg agaggtcact gggcctgttt				1920
tctccctcct gaccctgcat ctcccacccc gtgtatcata gggaactttc accttaaat				1980
ctttctaagc aaagtgtgaa taggattttt actccctttg tacagtattc tgagaaacgc				2040
aaataaaaagg gcaacatgtt tctg				2064

<210> 22  
 <211> 570  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (28) ... (489)

<400> 22	
agccggacgg ggatctgagc tggcagg atg aat gtg ggg gtg gca cac agc	51
	Met Asn Val Gly Val Ala His Ser
	1 5
gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg	99
Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu	
	10 15 20
gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc	147
Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile	
	25 30 35 40
ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat	195
Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His	
	45 50 55
aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt	243
Asn Leu Ala Thr Tyr Val Phe Leu His Thr Val Lys Gly Thr Pro Phe	
	16

	60		65		70	
gag act cct gac caa gga aag gct cgg cta ctg aca cac tgg gag caa						291
Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp Glu Gln						
	75		80		85	
atg gac tat ggg ctc cag ttt acc tct tcc cgc aag ttc ctc agc atc						339
Met Asp Tyr Gly Leu Gln Phe Thr Ser Ser Arg Lys Phe Leu Ser Ile						
	90		95		100	
tct cct att gtg ctc tat ctc ctg gcc agc ttc tat acc aag tat gat						387
Ser Pro Ile Val Leu Tyr Leu Leu Ala Ser Phe Tyr Thr Lys Tyr Asp						
	105		110		115	
gct gcg cac ttc ctc atc aac aca gcc tca ttg cta agt gta ctg ctg						435
Ala Ala His Phe Leu Ile Asn Thr Ala Ser Leu Leu Ser Val Leu Leu						
	125		130		135	
ccg aag ttg ccc cag ttc cat ggg gtt cgt gtc ttt ggc atc aac aaa						483
Pro Lys Leu Pro Gln Phe His Gly Val Arg Val Phe Gly Ile Asn Lys						
	140		145		150	
tac tgag ggatggggtt tgggacagct ccatgggcat ggggaaggca ctgaaacaga						540
Tyr						
ggactataaa acatccttct cttattctcc						570

<210> 23  
 <211> 1161  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (278)... (880)

<400> 23	
acatgagcca ccaaaatggt ggtgttcggg tatgaggctg ggactaagcc aagggattca	60
ggtgtggtgc cggtgggaac tgaggaagcg cccaaggaaa tgaaacacga tttccaaaat	120
gaacttaatc ttcatgaga aactgaggat agagatgtca ataagcagcc actgtttcca	180
cctccccacc tgaagagcta ggaggacaac tacaaagagc ctgactgcct tctcggaatg	240
aggagagagg aaaacagcaa cagtatcagt tttcaag atg gca gca tct atg	292
	Met Ala Ala Ser Met
	1 5
cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca	340
His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro	
	10 15 20
atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa	388
Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu	
	25 30 35
atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt	436
Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Ala Gly	
	40 45 50
ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag gtt	484
Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val	
	55 60 65
aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt	532
Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe	
	70 75 80 85
ttg tct act gtt gtt act gac aag ctt ttt gta att gat gct ttg tat	580
Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr	
	90 95 100
tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att	628
Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile	
	105 110 115
ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa	676
Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys	
	120 125 130
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa	724
	17

Asn	Gly	Arg	Leu	Ala	Thr	Lys	Tyr	His	Thr	Val	Pro	Leu	Pro	Pro	Lys	
	135					140					145					
gga	agg	gtt	tta	atc	cat	tgg	atg	acg	ctt	tgt	caa	aca	caa	atg	aaa	772
Gly	Arg	Val	Leu	Ile	His	Trp	Met	Thr	Leu	Cys	Gln	Thr	Gln	Met	Lys	
150					155					160					165	
tta	atg	gcg	att	cct	cta	gtc	ttt	cag	att	atg	ttt	gga	ata	tta	aat	820
Leu	Met	Ala	Ile	Pro	Leu	Val	Phe	Gln	Ile	Met	Phe	Gly	Ile	Leu	Asn	
				170					175					180		
ggt	cta	tac	cat	tat	gca	gta	ttt	gaa	gag	aca	ctt	gag	aaa	act	ata	868
Gly	Leu	Tyr	His	Tyr	Ala	Val	Phe	Glu	Glu	Thr	Leu	Glu	Lys	Thr	Ile	
			185					190					195			
cat	gaa	gag	taac	caaaaa	aatga	atggg	tgcta	actta	gcaaa	atgaa	ggt					920
His	Glu	Glu														
	200															
tctataa	aga	ggact	caggc	attgct	gaaa	gagtt	aaaag	taact	gtgaa	caaata	atatt					980
gttctgt	gcc	ttttgc	cctgg	tatatag	caa	atactc	aaaa	agtatt	caat	aattca	atca					1040
ataaat	tataa	gtttcat	ctt	acacgta	aga	tacagg	tctt	atctc	ctgat	ggtgtg	tcca					1100
ttttgc	cctgg	tatata	acag	ataata	aaata	tccagt	gtca	ataaat	gtaa	caataaa	agt					1160
t																1161

<210> 24  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (58) ... (627)

<400>	24															
acacacacat	ctgcac	ctca	accacag	act	acactt	gctg	aactgg	ctcc	tggggcc							57
atg	agg	ctg	tca	ctg	cca	ctg	ctg	ctg	ctg	ctg	gga	gcc	tgg	gcc		105
Met	Arg	Leu	Ser	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Trp	Ala		
1				5				10					15			
atc	cca	ggg	ggc	ctc	ggg	gac	agg	gcg	cca	ctc	aca	gcc	aca	gcc	cca	153
Ile	Pro	Gly	Gly	Leu	Gly	Asp	Arg	Ala	Pro	Leu	Thr	Ala	Thr	Ala	Pro	
			20					25					30			
caa	ctg	gat	gat	gag	gag	atg	tac	tca	gcc	cac	atg	ccc	gct	cac	ctg	201
Gln	Leu	Asp	Asp	Glu	Glu	Met	Tyr	Ser	Ala	His	Met	Pro	Ala	His	Leu	
			35				40					45				
cgc	tgt	gat	gcc	tgc	aga	gct	gtg	gct	tac	cag	atg	tgg	caa	aat	ctg	249
Arg	Cys	Asp	Ala	Cys	Arg	Ala	Val	Ala	Tyr	Gln	Met	Trp	Gln	Asn	Leu	
	50					55					60					
gca	aag	gca	gag	acc	aaa	ctt	cat	acc	tca	aac	tct	ggg	ggg	cgg	cgg	297
Ala	Lys	Ala	Glu	Thr	Lys	Leu	His	Thr	Ser	Asn	Ser	Gly	Gly	Arg	Arg	
	65				70					75					80	
gag	ctg	agc	gag	ttg	gtc	tac	acg	gat	gtc	ctg	gac	cgg	agc	tgc	tcc	345
Glu	Leu	Ser	Glu	Leu	Val	Tyr	Thr	Asp	Val	Leu	Asp	Arg	Ser	Cys	Ser	
				85					90					95		
cgg	aac	tgg	cag	gac	tac	gga	gtt	cga	gaa	gtg	gac	caa	gtg	aaa	cgt	393
Arg	Asn	Trp	Gln	Asp	Tyr	Gly	Val	Arg	Glu	Val	Asp	Gln	Val	Lys	Arg	
			100					105					110			
ctc	aca	ggc	cca	gga	ctt	agc	gag	ggg	cca	gag	cca	agc	atc	agc	gtg	441
Leu	Thr	Gly	Pro	Gly	Leu	Ser	Glu	Gly	Pro	Glu	Pro	Ser	Ile	Ser	Val	
		115					120					125				
atg	gtc	aca	ggg	ggc	ccc	tgg	cct	acc	agg	ctc	tcc	agg	aca	tgt	ttg	489
Met	Val	Thr	Gly	Gly	Pro	Trp	Pro	Thr	Arg	Leu	Ser	Arg	Thr	Cys	Leu	
	130					135					140					
cac	tac	ttg	ggg	gag	ttt	gga	gaa	gac	cag	atc	tat	gaa	gcc	cac	caa	537
His	Tyr	Leu	Gly	Glu	Phe	Gly	Glu	Asp	Gln	Ile	Tyr	Glu	Ala	His	Gln	
	145				150					155					160	
caa	ggc	cga	ggg	gct	ctg	gag	gca	ttg	cta	tgt	ggg	gga	ccc	cag	ggg	585
Gln	Gly	Arg	Gly	Ala	Leu	Glu	Ala	Leu	Leu	Cys	Gly	Gly	Pro	Gln	Gly	
										18						

	165		170		175	
gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc						630
Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu						
	180		185			
tggactctac cctcctctga aagaagctgg ggcttgctct gacggctctcc actcccgtct						690
gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccatcctgcc tccctcctcc						750
agcctcaggg cactcgggcc tgggtgggag tcaacgcctt cccctctgga ctcaaataaa						810
accagtgac ctc						823